

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 68.821 Seconds  
(without alignments)  
2392.073 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQFGRLVNTFSGVTNLFNSN.....EVDTPNDGFTPTFLASKIG 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	100.0	394	3	US-09-327-180-17
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3	2084	100.0	687	3	US-09-327-180-21
4	2084	100.0	687	5	US-10-612-668-21
5	2084	100.0	688	3	US-09-327-180-23
6	2084	100.0	688	5	US-10-612-668-23
7	1837	88.1	752	3	US-09-327-180-2
8	1837	88.1	752	5	US-10-612-668-2
9	1234.5	59.2	667	4	US-10-108-260A-3778
10	494.5	23.7	877	6	US-11-097-143-14664
11	324	15.5	1330	4	US-10-108-260A-3237
12	313.5	15.0	1549	6	US-11-097-143-1776
13	313.5	15.0	1549	6	US-11-097-143-29028
14	302.5	14.5	2443	6	US-11-097-143-8355
15	301	14.4	786	4	US-10-164-080-2
16	301	14.4	786	4	US-10-299-327-2
17	301	14.4	786	4	US-10-128-174-13
18	301	14.4	786	4	US-10-128-174-31
19	301	14.4	786	4	US-10-128-174-32
20	301	14.4	786	4	US-10-128-174-33
21	301	14.4	787	3	US-09-866-050A-334
22	300.5	14.4	347	4	US-10-128-174-30
23	300.5	14.4	1724	3	US-09-364-899-43
24	300.5	14.4	1724	5	US-10-975-523-43
25	296	14.2	1094	5	US-10-479-764-22
26	296	14.2	1097	5	US-10-450-763-52300
27	296	14.2	3913	4	US-10-334-143-45

28	296	14.2	4274	5	US-10-450-763-31331	Sequence 31331, A
29	296	14.2	4377	5	US-10-756-149-4917	Sequence 4917, Ap
30	296	14.2	4386	5	US-10-450-763-37734	Sequence 37734, A
31	296	14.2	4397	5	US-10-450-763-52303	Sequence 52303, A
32	288	13.8	1762	4	US-10-205-194-117	Sequence 117, Appl
33	283.5	13.6	784	4	US-10-164-080-7	Sequence 7, Appl
34	283.5	13.6	784	4	US-10-258-951-70	Sequence 70, Appl
35	283.5	13.6	784	5	US-10-923-035-56	Sequence 56, Appl
36	283.5	13.6	784	5	US-10-990-000-70	Sequence 70, Appl
37	281.5	13.5	784	4	US-10-354-358-38	Sequence 38, Appl
38	281.5	13.5	784	4	US-10-128-174-12	Sequence 12, Appl
39	281.5	13.5	784	4	US-10-658-904-2	Sequence 2, Appl
40	280.5	13.5	720	4	US-10-433-794-20	Sequence 20, Appl
41	280.5	13.5	765	4	US-10-128-174-3	Sequence 3, Appl
42	280.5	13.5	765	4	US-10-128-174-34	Sequence 34, Appl
43	280.5	13.5	765	4	US-10-128-174-35	Sequence 35, Appl
44	280.5	13.5	765	4	US-10-128-174-36	Sequence 36, Appl
45	280.5	13.5	765	4	US-10-128-174-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1  
US-09-327-180-17  
; Sequence 17, Application US/09927180  
; Patent No. US2002010634A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-327-180-17

Query Match 100.0%; Score 2084; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 6.5e-191;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREGQLILFQNTPNRTWDCVLV 60  
Db 1 MQFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGFRLFOLEADALVNFHOYSSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120  
DB 61 NPRNSQSGFRLFOLEADALVNFHOYSSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYKGETVHYAVQDQNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVHYAVQDQNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
DB 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDGETPTFLASKIG 394  
DB 361 DNVEMIKALIVFGAEVDTNDGETPTFLASKIG 394

RESULT 2  
US-10-612-668-17  
; Sequence 17, Application US/10612668  
; Publication NO. US20050196852A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/612,668  
; FILING DATE: 01-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-612-668-17  
Query Match 100.0%; Score 2084; DB 5; Length 394;  
Best Local Similarity 100.0%; Pred. No. 6.5e-191;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MOFFRLVNTFSGVTNLFSPNFRVKEVAVADYTSDDRVEEGQLILFQNTNRTWDCVLV 60  
QY 61 NPRNSQSGFRLFOLEADALVNFHOYSSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120  
DB 61 NPRNSQSGFRLFOLEADALVNFHOYSSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPWS 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYKGETVHYAVQDQNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVHYAVQDQNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
DB 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDGETPTFLASKIG 394  
DB 361 DNVEMIKALIVFGAEVDTNDGETPTFLASKIG 394  
RESULT 3  
US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-927-180-21

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 8.60262 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQPFGRLVNTFSGVTNLFNS.....EVDTPNDGFTPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 2862289 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:  
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4: /cgn2\_6/ptodata/1/pubpaa/BCT\_NEW\_PUB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	14.9	1159	6	US-10-055-877-139
2	296	14.2	4384	6	US-10-821-234-1120
3	293	14.1	1765	6	US-10-055-877-140
4	293	14.1	1940	6	US-10-055-877-141
5	278.5	13.4	784	7	US-11-072-175-153
6	271.5	13.0	1059	6	US-10-055-877-138
7	249	11.9	791	6	US-10-055-877-137
8	244	11.7	237	7	US-11-096-568A-28113
9	244	11.7	247	7	US-11-096-568A-28112
10	234	11.2	1431	6	US-10-501-035-220
11	231	11.1	795	7	US-11-072-512-2378
12	230	11.0	993	6	US-10-055-877-6
13	229.5	11.0	240	7	US-11-096-568A-22417
14	229.5	11.0	244	7	US-11-096-568A-22416
15	227.5	10.9	645	7	US-11-072-512-2588
16	223	10.7	219	7	US-11-096-568A-28114
17	219.5	10.5	505	7	US-11-072-512-2553
18	213	10.2	241	7	US-11-096-568A-9945
19	213	10.2	245	7	US-11-096-568A-9944
20	213	10.2	280	7	US-11-096-568A-9943
21	206.5	9.9	657	7	US-11-072-512-2529
22	204	9.8	835	7	US-11-072-512-2529
23	202	9.7	2471	7	US-11-050-346-68
24	200	9.6	656	7	US-11-234-786-379
25	200	9.6	671	7	US-11-234-786-380

Sequence 378, App  
Sequence 67, Appl  
Sequence 376, App  
Sequence 2, Appl  
Sequence 532, App  
Sequence 16312, A  
Sequence 16312, A  
Sequence 11369, A  
Sequence 11368, A  
Sequence 11367, A  
Sequence 975, App  
Sequence 10314, A  
Sequence 10313, A  
Sequence 219, App  
Sequence 2283, App  
Sequence 3095, App  
Sequence 377, App  
Sequence 12768, A  
Sequence 12767, A

US-11-234-786-378  
US-11-050-346-67  
US-11-234-786-376  
US-11-050-346-67  
US-11-072-512-2675  
US-11-234-786-532  
US-11-096-568A-16313  
US-11-096-568A-16312  
US-11-096-568A-11369  
US-11-096-568A-11368  
US-11-096-568A-11367  
US-10-821-234-975  
US-11-096-568A-10314  
US-11-096-568A-10313  
US-10-501-035-219  
US-11-072-512-2283  
US-11-072-512-3095  
US-11-234-786-377  
US-11-096-568A-12768  
US-11-096-568A-12767

## ALIGNMENTS

## RESULT 1

US-10-055-877-139

Sequence 139, Application US/10055877

Publication No. US20050288241A1

## GENERAL INFORMATION:

APPLICANT: DeCristofaro, Marc  
APPLICANT: Padigaru, Muraidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchervnev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytek, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
PRIOR FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-877-139

Query Match      14.9%; Score 310; DB 6; Length 1159;
Best Local Similarity 27.8%; Pred. No. 1.7e-21;
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

QY 103 HTEVLQHTDLIRNPS-----MSVAHLA-----VEIGRECFHSHRSIIISCANCA 147
DB 349 HVRVAKLLD--RNADANARALNGFTPLHIACKNRLKVVELLR---HGASIS---A 398
QY 148 ENEECTPLHLACRGDGEILLVELVQYCHTQMDVTDYKGTVFHYAVQGDNSQVQLLGR 207
DB 399 TTESGLTPLHVAAFGCMNVIVYLQH--DASPDVPTVRGTGTPHLHAAANQTDIIRILLR 457
QY 208 NAVAGLNQVNNGLTPLHLACQLGKQEMVRVLLLCNARCN----- 247
DB 458 NG-AQVDARAREQQTPLHIAASRLGNVDIVMLLQHGQVDATTCKMYTALHIAAKECODE 516
QY 248 ---IMPNG-----YPIHSAKFSQKCAEMIISMDSQIHSKDPKPYGASPLHW 293
DB 517 VAAVLIENGALDAATKKGFTPLHLTKYGHKVAQLLQKEADV--DAQGKNGVTPLHV 574
QY 294 A---KNAEWARMLLKRCGNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHG 350
DB 575 ACHYNNQVALLLEKSGASPHATKNGHTPLHIAARKNQMDTATTLLEYGALANAESKAG 634
QY 351 NTPHLHANSKONVEMIKALIVFGAEVDPDNDFTPTFLASK 392
DB 635 FTPLHLSQEGHAEISNLLIEHKAAVNHPAKNGLTPLMLCAQ 676

RESULT 2
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Ton
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match      14.2%; Score 296; DB 6; Length 4384;
Best Local Similarity 29.2%; Pred. No. 2.6e-19;

; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-877-139

Query Match      14.9%; Score 310; DB 6; Length 1159;
Best Local Similarity 27.8%; Pred. No. 1.7e-21;
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

QY 103 HTEVLQHTDLIRNPS-----MSVAHLA-----VEIGRECFHSHRSIIISCANCA 147
DB 349 HVRVAKLLD--RNADANARALNGFTPLHIACKNRLKVVELLR---HGASIS---A 398
QY 148 ENEECTPLHLACRGDGEILLVELVQYCHTQMDVTDYKGTVFHYAVQGDNSQVQLLGR 207
DB 399 TTESGLTPLHVAAFGCMNVIVYLQH--DASPDVPTVRGTGTPHLHAAANQTDIIRILLR 457
QY 208 NAVAGLNQVNNGLTPLHLACQLGKQEMVRVLLLCNARCN----- 247
DB 458 NG-AQVDARAREQQTPLHIAASRLGNVDIVMLLQHGQVDATTCKMYTALHIAAKECODE 516
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DB 517 VAAVLIENGALDAATKKGFTPLHLTKYGHKVAQLLQKEADV--DAQGKNGVTPLHV 574
QY 294 A---KNAEWARMLLKRCGNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGEHG 350
DB 575 ACHYNNQVALLLEKSGASPHATKNGHTPLHIAARKNQMDTATTLLEYGALANAESKAG 634
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DB 635 FTPLHLSQEGHAEISNLLIEHKAAVNHPAKNGLTPLMLCAQ 676

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; Sequence 140, Application US/10055877
; Publication No. US20050289241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zehusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Perence
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 20.4551 Seconds  
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1592.473 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQFFGLVNTSGVTNLFNS.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62  
Gapop: 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2084	100.0	394	2	US-09-519-223-17
4	2084	100.0	687	1	US-08-555-568B-21
5	2084	100.0	687	2	US-09-519-223-21
6	2084	100.0	687	2	US-09-519-223-21
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9	2084	100.0	688	2	US-09-519-223-23
10	2078	99.7	819	2	US-09-519-223-23
11	1837	88.1	752	1	US-08-281-193-2
12	1837	88.1	752	1	US-08-422-106-2
13	1837	88.1	752	1	US-08-735-716-2
14	1837	88.1	752	1	US-08-555-568B-2
15	1837	88.1	752	2	US-09-519-223-2
16	1837	88.1	752	2	US-09-519-223-2
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19	359.5	17.3	545	2	US-09-270-767-61684
20	338	16.2	843	1	US-09-172-977-3
21	338	16.2	843	3	US-09-404-108-3
22	332	15.9	1839	1	US-09-172-977-4
23	332	15.9	1839	2	US-09-404-108-4
24	332	15.9	2753	2	US-09-519-223-2
25	332	15.9	2753	2	US-09-519-223-2
26	332	15.9	3924	2	US-09-519-223-2
27	305.5	14.7	1745	1	US-09-031-485-33

28	305.5	14.7	1745	1	US-08-847-429A-33	Sequence 33, Appl
29	305.5	14.7	1745	2	US-09-065-474-33	Sequence 33, Appl
30	305.5	14.7	1745	2	US-09-557-034-33	Sequence 33, Appl
31	301	14.4	786	2	US-09-509-802-2	Sequence 2, Appli
32	301	14.4	787	2	US-09-188-930-334	Sequence 334, App
33	301	14.4	787	2	US-09-312-283C-334	Sequence 334, App
34	300.5	14.4	1724	2	US-09-964-899-43	Sequence 43, Appl
35	296	14.2	1088	2	US-09-082-059-2	Sequence 2, Appli
36	296	14.2	3913	2	US-09-949-016-10973	Sequence 10973, A
37	296	14.2	4377	2	US-09-949-016-6978	Sequence 6978, Ap
38	294	14.1	1719	2	US-09-949-016-6966	Sequence 6966, Ap
39	294	14.1	1856	2	US-09-949-016-5876	Sequence 5876, Ap
40	294	14.1	1880	2	US-09-949-016-5876	Sequence 5876, Ap
41	294	14.1	1881	2	US-09-949-016-5876	Sequence 5876, Ap
42	294	14.1	1883	2	US-09-949-016-9010	Sequence 9010, Ap
43	294	14.1	1883	2	US-09-949-016-9011	Sequence 9011, Ap
44	294	14.1	1883	2	US-09-949-016-9012	Sequence 9012, Ap
45	294	14.1	1883	2	US-09-949-016-9013	Sequence 9013, Ap

ALIGNMENTS

RESULT 1  
US-08-555-568B-17  
; Sequence 17, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-17

Query Match	100.0%;	Score 2084;	DB 1;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 2.4e-226;	Mismatches 0;	Indels 0;
Matches 394;	Conservative 0;			
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Db	1	MOFFGLVNTSGVTNLFNSFRVKEVAVADYSSDRVREEGQLILFQNTPNRTMDCVLV	60	
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DB 121 SVAHLAVELGIRECFPHSRISIIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYKGETVFHYAVQDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVFHYAVQDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCNIMGNGPYPIHSAMKFSQKCAEMIISMDSOQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIMGNGPYPIHSAMKFSQKCAEMIISMDSOQIHSKDPYRGASPLHWAKNAEMA 300  
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DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRNFDCAI VLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNPDTFETFLASKIG 394  
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RESULT 2

US-09-519-223-17  
; Sequence 17, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-519-223-17

Query Match 100.0%; Score 2084; DB 2; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2.4e-226;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60  
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DB 121 SVAHLAVELGIRECFPHSRISIIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYKGETVFHYAVQDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
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DB 241 LCNARCNIMGNGPYPIHSAMKFSQKCAEMIISMDSOQIHSKDPYRGASPLHWAKNAEMA 300  
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DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRNFDCAI VLLTHGANADARGEHNTPLHLAMSK 360  
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RESULT 3

US-09-927-180-17  
; Sequence 17, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 2; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2.4e-226;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60  
DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60  
QY 61 NPNRSQSGFRLQLEADALVNFHQYSSQLLPFYESSPQVLHTEVLOHLDLIRNHPSW 120

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: March 22, 2006, 12:00:11 ; Search time 51.0044 Seconds  
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Title: US-10-612-668-19

Perfect score: 1531

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications\_AA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1531	100.0	688	3	US-09-927-180-23
6	1531	100.0	688	5	US-10-612-668-23
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10	736	48.1	877	6	US-11-097-143-14664
11	456.5	29.8	1071	4	US-10-369-493-6885
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13	419	27.4	1023	4	US-10-369-493-6690
14	261	17.0	468	4	US-10-369-493-4998
15	245	16.0	1053	4	US-10-425-115-196524
16	235	15.3	1254	4	US-10-437-963-169583
17	234	15.3	387	4	US-10-421-654-66
18	234	15.3	387	5	US-10-796-907-66
19	211.5	13.8	370	3	US-09-925-300-1483
20	211.5	13.8	562	5	US-10-786-505-21
21	211.5	13.8	661	5	US-10-786-505-18
22	211.5	13.8	682	5	US-10-181-069-9
23	211.5	13.8	682	5	US-10-786-505-15
24	211.5	13.8	782	5	US-10-786-505-1
25	208.5	13.6	350	4	US-10-421-654-100
26	208.5	13.6	350	5	US-10-796-907-100
27	207.5	13.6	308	5	US-10-796-907-132

28 204.5 13.4 577 4 US-10-310-154-616 Sequence 616, App  
29 201 13.1 315 4 US-10-424-599-259117 Sequence 259117,  
30 201 13.1 382 4 US-10-310-154-615 Sequence 615, App  
31 195.5 12.8 382 4 US-10-424-599-258423 Sequence 258423,  
32 193.5 12.6 387 4 US-10-437-963-177823 Sequence 177823,  
33 190 12.4 378 4 US-10-421-654-18 Sequence 18, Appl  
34 190 12.4 378 5 US-10-796-907-18 Sequence 18, Appl  
35 182 11.9 37 6 US-11-028-376-13 Sequence 13, Appl  
36 182 11.9 37 6 US-11-010-558-6 Sequence 6, Appli  
37 178 11.6 435 4 US-10-425-115-343159 Sequence 343159,  
38 177 11.6 410 3 US-09-755-630A-290 Sequence 290, App  
39 177 11.6 410 3 US-09-755-630A-292 Sequence 292, App  
40 177 11.6 410 5 US-10-658-180-290 Sequence 290, App  
41 177 11.6 410 5 US-10-658-180-292 Sequence 292, App  
42 177 11.6 410 5 US-10-682-011-10 Sequence 10, Appl  
43 177 11.6 410 5 US-10-682-011-12 Sequence 12, Appl  
44 177 11.6 434 4 US-10-425-114-39447 Sequence 39447, A  
45 177 11.6 437 4 US-10-425-114-39376 Sequence 39376, A

#### ALIGNMENTS

#### RESULT 1

US-09-927-180-19

; Sequence 19, Application US/09927180

; Patent No. US20020106364A1

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; TANG, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA: US/09/927,180

; FILING DATE: 09-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/519,223

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 292 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-927-180-19

Query Match 100.0%; Score 1531; DB 3; Length 292;  
Best Local Similarity 100.0%; Pred No. 4, 1e-152;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 LODLMIHSRARKPAFLGSMRDKRTHLLCLDGGVKGKGLIIIIQLLIAIEKASGVATKD 60

QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 120  
DB 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 120  
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DB 121 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
QY 181 WRAARSSGAAPTFRPNRFLDGLGILLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIV 240  
DB 181 WRAARSSGAAPTFRPNRFLDGLGILLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292  
DB 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

## RESULT 2

US-10-612-668-19  
; Sequence 19, Application US/10612668  
; Publication No. US20050196852A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/612,668  
FILING DATE: 01-Jul-2003  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180  
FILING DATE: 09-Aug-2001  
APPLICATION NUMBER: 09/519,223  
FILING DATE: 01-Jul-2003

## ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-612-668-19

Query Match 100.0%; Score 1531; DB 5; Length 292;  
Best Local Similarity 100.0%; Pred. No. 4.1e-152;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIHSRARKPAFILGSMRDEKTRHLLCLDGGVKGKLIIOILLIAIEKASGVATKD 60  
DB 1 LQDLMIHSRARKPAFILGSMRDEKTRHLLCLDGGVKGKLIIOILLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 120

DB 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
DB 121 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
QY 181 WRAARSSGAAPTFRPNRFLDGLGILLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIV 240  
DB 181 WRAARSSGAAPTFRPNRFLDGLGILLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292  
DB 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

## RESULT 3

US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/927,180  
FILING DATE: 09-Aug-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223  
FILING DATE: <Unknown>

## ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:  
LENGTH: 687 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-927-180-21

Query Match 100.0%; Score 1531; DB 3; Length 687;  
Best Local Similarity 100.0%; Pred. No. 1.4e-151;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 396 LQDLMIHSRARKPAFILGSMRDEKTRHLLCLDGGVKGKLIIOILLIAIEKASGVATKD 455  
QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 120  
DB 456 LFDWVAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVRGSRPYESGLEFLKREFGE 515  
QY 121 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
DB 516 HTKMTDVRKPKVMTLGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 6.37555 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMHISRAKPAFLGSM.....CAKELGKMWVDCCTDPGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New\*

1: /cgn2\_6/ptodata/1/pubpa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubpa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpa/PCT\_NEW\_PUB pep.\*  
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6: /cgn2\_6/ptodata/1/pubpa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/1/pubpa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubpa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
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2	233	15.2	784	7	US-11-096-568A-1543
3	207	13.5	779	7	US-11-096-568A-1544
4	206.5	13.5	380	7	US-11-096-568A-3088
5	206.5	13.5	380	7	US-11-096-568A-3091
6	201	13.1	382	7	US-11-096-568A-32354
7	201	13.1	384	7	US-11-096-568A-32353
8	173	11.3	400	7	US-11-195-968-1
9	155.5	10.2	406	7	US-11-195-968-12
10	147	9.6	526	7	US-11-096-568A-34163
11	138.5	9.0	297	7	US-11-096-568A-3089
12	132.5	8.7	288	7	US-11-096-568A-32355
13	129.5	8.5	391	7	US-11-058-727-123
14	129.5	8.5	391	7	US-11-108-389-123
15	129.5	8.5	391	7	US-11-224-624-123
16	125	8.2	391	7	US-11-058-727-119
17	125	8.2	391	7	US-11-058-727-121
18	125	8.2	391	7	US-11-108-389-119
19	125	8.2	391	7	US-11-108-389-121
20	125	8.2	391	7	US-11-224-624-119
21	125	8.2	391	7	US-11-224-624-121
22	124.5	8.1	249	7	US-11-096-568A-3090
23	122.5	8.0	454	7	US-11-096-568A-18178
24	122.5	8.0	460	7	US-11-096-568A-18177
25	117	7.6	396	7	US-11-096-568A-34164

26 111.5 7.3 381 7 US-11-096-568A-34165  
27 85 5.6 467 7 US-11-072-512-2838  
28 84.5 5.5 348 7 US-11-087-099-10729  
29 84 5.5 360 7 US-11-096-568A-27737  
30 84 5.5 394 7 US-11-096-568A-27736  
31 84 5.5 482 7 US-11-096-568A-27735  
32 83 5.4 591 7 US-11-098-686-11119  
33 82 5.4 558 6 US-10-467-657-4258  
34 81.5 5.3 619 7 US-11-210-471-4  
35 80.5 5.3 619 7 US-11-210-471-10  
36 80.5 5.3 3588 6 US-10-995-561-672  
37 80.5 5.3 4346 6 US-10-995-561-671  
38 80.5 5.3 4347 6 US-10-995-561-670  
39 80.5 5.3 4390 7 US-11-169-041-169  
40 80.5 5.3 4419 6 US-10-821-234-1155  
41 79.5 5.2 330 7 US-11-087-059-8291  
42 79 5.2 228 7 US-11-052-554A-366  
43 79 5.2 359 6 US-10-467-657-1650  
44 79 5.2 1377 6 US-10-821-234-1070  
45 78.5 5.1 310 7 US-11-096-568A-27488

## ALIGNMENTS

## RESULT 1

US-11-096-568A-1542  
; Sequence 1542, Application US/11096568A  
; Publication No. US20060048240A1

; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide

; TITLE OF INVENTION: Therby

; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471

; SEQ ID NO 1542

; LENGTH: 831

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(831)

; OTHER INFORMATION: Ceres Seq. ID no. 14313476

US-11-096-568A-1542

Query Match 15.5%; Score 238; DB 7; Length 831;  
Best Local Similarity 26.8%; Pred. No. 6.8e-15;  
Matches 77; Conservative 40; Mismatches 84; Indels 86; Gaps 10;

QY 30 LCLDGGVKGKLIILQILIAIEKASGVATKDLFDWAGTGTGILALAI-LHKSMAVMR 88  
Db 45 ILSMDGGMKGLATVQMLKQIEQGTGKRIHEMFDLICGTSTGGMLMALGDKMTLDQCE 104  
QY 89 GMTFRM-----KDE-----VFGRSRVYESGPLEEPLKR- 116  
Db 105 EITKLGKLVFAPIPKDEATWKEKLDQLFKSSSSQFRVVVHGSK-HSADQFERLLKEM 163  
QY 117 ---EFGHTKMTDVRK-PKVMLTGTLSDROPALHLFRNYDAPETVREPRFNQMVNLRPP 172  
Db 164 CADEDGDLIESAVKGIKPKVFAVSLVSVMPAQPIFRNYQYPPGTLE-----VSPG 215  
QY 173 AQSDQI-----WRAARSSGAAPTFR-----PNGRFLD 202  
Db 216 MAEPPSISAITAVSGAPVGIKRGAPMGSKRWWEAIRASSAAPPYVLDYDFSDANRQWD 275  
QY 203 GGLANNPTLDAMTETHEYNQDLIRKGOANKVKLSIVSLGTGRSP 249  
Db 276 GAIVANNPTIFAIREAQLLPD-----TRIDCLVSGCGSVP 312

## RESULT 2



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM.protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 15.1596 Seconds  
(without alignments)  
1592.473 Million cell updates/sec

Title: US-10-612-668-19  
Perfect score: 1531  
Sequence: 1 LQDLMHISARKPAFLGSM.....GAKELGRQVVDCTDPDGRP 292

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1531	100.0	292	1	US-08-555-568B-19
2	1531	100.0	292	2	US-09-519-223-19
3	1531	100.0	292	2	US-09-927-180-19
4	1531	100.0	687	1	US-08-555-568B-21
5	1531	100.0	687	2	US-09-519-223-21
6	1531	100.0	687	2	US-09-927-180-21
7	1531	100.0	688	1	US-08-555-568B-23
8	1531	100.0	688	2	US-09-519-223-23
9	1531	100.0	688	2	US-09-927-180-23
10	1524	99.5	819	2	US-09-949-016-10948
11	1471	96.1	752	1	US-08-281-193-2
12	1471	96.1	752	1	US-08-422-106-2
13	1471	96.1	752	1	US-08-735-716-2
14	1471	96.1	752	1	US-08-555-568B-2
15	1471	96.1	752	1	US-09-519-223-2
16	1471	96.1	752	2	US-09-927-180-2
17	1471	96.1	752	4	PCT-US95-08069-2
18	736	48.1	896	2	US-09-270-767-46130
19	610	39.8	545	2	US-09-270-767-61684
20	371	24.2	143	2	US-09-270-767-33298
21	177	11.6	410	2	US-09-755-630B-290
22	177	11.6	410	2	US-09-755-630B-292
23	177	11.6	410	2	US-09-755-274-10
24	177	11.6	410	2	US-09-755-274-12
25	177	11.6	410	2	US-10-658-180-290
26	177	11.6	410	2	US-10-658-180-292
27	175	11.4	337	2	US-09-755-630B-293

28	175	11.4	337	2	US-09-755-274-13	Sequence 13, Appl
29	175	11.4	337	2	US-10-658-180-293	Sequence 293, App
30	175	11.4	410	1	US-08-449-986-2	Sequence 2, Appli
31	175	11.4	410	1	US-08-756-855-2	Sequence 2, Appli
32	175	11.4	410	2	US-09-755-630B-288	Sequence 288, App
33	175	11.4	410	2	US-09-755-630B-291	Sequence 291, App
34	175	11.4	410	2	US-09-755-274-11	Sequence 11, Appl
35	175	11.4	410	2	US-09-755-274-11	Sequence 11, Appl
36	175	11.4	410	2	US-10-658-180-288	Sequence 288, App
37	175	11.4	410	2	US-10-658-180-291	Sequence 291, App
38	175	11.4	508	2	US-09-755-630B-289	Sequence 289, App
39	175	11.4	508	2	US-09-755-274-9	Sequence 9, Appli
40	175	11.4	508	2	US-10-658-180-289	Sequence 289, App
41	142.5	9.3	383	1	US-07-936-163-4	Sequence 4, Appli
42	140	9.1	381	1	US-07-936-163-3	Sequence 3, Appli
43	140	9.1	386	2	US-09-755-630B-278	Sequence 278, App
44	140	9.1	386	2	US-09-755-274-5	Sequence 5, Appli
45	140	9.1	386	2	US-10-658-180-278	Sequence 278, App

ALIGNMENTS

RESULT 1  
US-08-555-568B-19  
; Sequence 19, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-19

Query Match	100.0%	Score 1531	DB 1	Length 292
Best Local Similarity	100.0%	Pred. No. 2.4e-167	Indels 0	Gaps 0
Matches 292	Conservative 0	Mismatches 0		
QY	1	LQDLMHISARKPAFLGSMRDEKTRHLLCLDGGVKGKGLIIQLLIAIEKASGVATKD	60	
Db	1	LQDLMHISARKPAFLGSMRDEKTRHLLCLDGGVKGKGLIIQLLIAIEKASGVATKD	60	
QY	61	LFDWVAGTGTGILAILHLHKSMAVMRGMYFRMKDEVFRGSPYSGPLEEFLKREFGE	120	
Db	61	LFDWVAGTGTGILAILHLHKSMAVMRGMYFRMKDEVFRGSPYSGPLEEFLKREFGE	120	

QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240  
Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240  
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Db 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVMVDDCCTDDPGRP 292

## RESULT 2

US-09-519-223-19  
; Sequence 19, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-519-223-19  
Query Match 100.0%; Score 1531; DB 2; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2.4e-167;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQDLMHISARKPAFILGSMRDEKTRHDHLLCLDGGVKGGLIIIIQLLIAIEKASGVATKD 60  
Db 1 LQDLMHISARKPAFILGSMRDEKTRHDHLLCLDGGVKGGLIIIIQLLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120  
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240

US-09-519-223-19  
Query Match 100.0%; Score 1531; DB 2; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2.4e-167;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQDLMHISARKPAFILGSMRDEKTRHDHLLCLDGGVKGGLIIIIQLLIAIEKASGVATKD 60  
Db 1 LQDLMHISARKPAFILGSMRDEKTRHDHLLCLDGGVKGGLIIIIQLLIAIEKASGVATKD 60  
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Db 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240

Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVMVDDCCTDDPGRP 292  
Db 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVMVDDCCTDDPGRP 292

## RESULT 3

US-09-927-180-19  
; Sequence 19, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 2; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2.4e-167;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 LQDLMHISARKPAFILGSMRDEKTRHDHLLCLDGGVKGGLIIIIQLLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120  
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240  
Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVMVDDCCTDDPGRP 292

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 120 Seconds  
(without alignments)  
2392.073 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFSGVTLNFSN.....GAKELGRWVVDCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3620	100.0	687	3	US-09-927-180-21
2	3620	100.0	687	5	US-10-612-668-21
3	3606.5	99.6	688	3	US-09-927-180-23
4	3606.5	99.6	688	5	US-10-612-668-23
5	3302.5	91.2	752	3	US-09-927-180-2
6	3302.5	91.2	752	5	US-10-612-668-2
7	2723	75.2	667	4	US-10-108-260A-3778
8	2084	57.6	394	3	US-09-927-180-17
9	2084	57.6	394	5	US-10-612-668-17
10	1531	42.3	292	3	US-09-927-180-19
11	1531	42.3	292	5	US-10-612-668-19
12	1163.5	32.1	877	6	US-11-097-143-14664
13	647.5	17.9	1071	4	US-10-369-493-6865
14	634.5	17.5	1023	4	US-10-369-493-6689
15	634.5	17.5	1023	4	US-10-369-493-6690
16	324.5	9.0	468	4	US-10-369-493-4998
17	324	9.0	1330	4	US-10-108-260A-3237
18	320	8.8	1549	6	US-11-097-143-1776
19	320	8.8	1549	6	US-11-097-143-29028
20	302.5	8.4	2443	6	US-11-097-143-8355
21	302	8.3	786	4	US-10-164-080-2
22	302	8.3	786	4	US-10-299-327-2
23	302	8.3	786	4	US-10-128-174-13
24	302	8.3	786	4	US-10-128-174-31
25	302	8.3	786	4	US-10-128-174-32
26	302	8.3	786	4	US-10-128-174-33
27	302	8.3	787	3	US-09-866-050A-334

28	301.5	8.3	347	4	US-10-128-174-30	Sequence 30, Appl
29	300.5	8.3	1724	3	US-09-964-899-43	Sequence 43, Appl
30	300.5	8.3	1724	5	US-10-975-523-43	Sequence 43, Appl
31	300	8.3	1762	4	US-10-205-194-117	Sequence 117, Appl
32	296	8.2	1094	5	US-10-479-764-22	Sequence 22, Appl
33	296	8.2	1097	5	US-10-450-763-52300	Sequence 52300, A
34	296	8.2	3913	4	US-10-334-143-45	Sequence 45, Appl
35	296	8.2	4274	5	US-10-450-763-31331	Sequence 31331, A
36	296	8.2	4377	5	US-10-756-149-4917	Sequence 4917, Ap
37	296	8.2	4386	5	US-10-450-763-37734	Sequence 37734, A
38	296	8.2	4397	5	US-10-450-763-52303	Sequence 52303, A
39	290	8.0	720	4	US-10-433-794-20	Sequence 20, Appl
40	290	8.0	765	4	US-10-128-174-3	Sequence 3, Appli
41	290	8.0	765	4	US-10-128-174-34	Sequence 34, Appl
42	290	8.0	765	4	US-10-128-174-35	Sequence 35, Appl
43	290	8.0	765	4	US-10-128-174-36	Sequence 36, Appl
44	290	8.0	785	4	US-10-128-174-37	Sequence 37, Appl
45	290	8.0	765	4	US-10-128-174-38	Sequence 38, Appl

## ALIGNMENTS

### RESULT 1

US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; ; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/09/927,180  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 876-5851  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTLNFSNPFVKEVAADYTTSSDRVREEGQLILFQNTPNRTDCVLV 60

DB 1 MQFFGLVNTFSGVTLNFSNPFVKEVAADYTTSSDRVREEGQLILFQNTPNRTDCVLV 60

QY 61 NPRNSQSGRLFOLEADALVNFHQYSSQLLPYESSPOVLHTEVLQHLTDLIRNHPW 120  
DB 61 NPRNSQSGRLFOLEADALVNFHQYSSQLLPYESSPOVLHTEVLQHLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKOPRYGASPLHWAKNAEMA 300  
DB 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKOPRYGASPLHWAKNAEMA 300  
QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGKQLDLMIHSRARKPAFILGSMRDEKR 420  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGKQLDLMIHSRARKPAFILGSMRDEKR 420  
QY 421 THDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
DB 421 THDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
QY 481 YNRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSRQPAE 540  
DB 481 YNRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSRQPAE 540  
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DB 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660  
QY 661 ELAKTVFGAKELGKMVVDCCDTPDGRP 687  
DB 661 ELAKTVFGAKELGKMVVDCCDTPDGRP 687

## RESULT 2

US-10-612-668-21

Sequence 21, Application US/10612668

Publication No. US20050196852A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/10/612,668

APPLICATION NUMBER: US/10/612,668

FILING DATE: 01-Jul-2003

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

APPLICATION NUMBER: 09/519,223

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-612-668-21

Query Match 100.0%; Score 3620; DB 5; Length 687;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFGVNTLFSNPRVKEVAVADYTSRVRREEGQLILFQNTPNRTWDCVLV 60

DB 1 MOFFGLVNTFGVNTLFSNPRVKEVAVADYTSRVRREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPYESSPOVLHTEVLQHLTDLIRNHPW 120

DB 61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPYESSPOVLHTEVLQHLTDLIRNHPW 120

QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180

DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180

QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240

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QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKOPRYGASPLHWAKNAEMA 300

DB 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKOPRYGASPLHWAKNAEMA 300

QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGKQLDLMIHSRARKPAFILGSMRDEKR 420

DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGKQLDLMIHSRARKPAFILGSMRDEKR 420

QY 421 THDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480

DB 421 THDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480

QY 481 YNRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSRQPAE 540

DB 481 YNRGMVFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSRQPAE 540

QY 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDOLVWRAARSSGAAPTYFRPNRGRFLDGG 600

DB 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDOLVWRAARSSGAAPTYFRPNRGRFLDGG 600

QY 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660

DB 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660

QY 661 ELAKTVFGAKELGKMVVDCCDTPDGRP 687

DB 661 ELAKTVFGAKELGKMVVDCCDTPDGRP 687

## RESULT 3

US-09-927-180-23

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 15 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFGRLVNTSGVTLNFSN.....GAKELGKXVVDCTDPGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US03\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	296	8.2	4384	6	US-10-821-234-1120
3	294.5	8.1	1765	6	US-10-055-877-140
4	294.5	8.1	1940	6	US-10-055-877-141
5	279.5	7.7	784	7	US-11-072-175-153
6	278.5	7.7	1059	6	US-10-055-877-138
7	264	7.3	1431	6	US-10-501-035-220
8	251.5	6.9	795	7	US-11-072-512-2378
9	249	6.9	791	6	US-10-055-877-137
10	244	6.7	237	7	US-11-096-568A-28113
11	244	6.7	247	7	US-11-096-568A-28112
12	238	6.6	831	6	US-11-096-568A-1542
13	234	6.5	993	6	US-10-055-877-6
14	233	6.4	784	7	US-11-096-568A-1543
15	230	6.4	645	7	US-11-072-512-2588
16	229.5	6.3	240	7	US-11-096-568A-22417
17	229.5	6.3	244	7	US-11-096-568A-22416
18	225.5	6.2	505	7	US-11-072-512-2553
19	223	6.2	219	7	US-11-096-568A-28114
20	215	5.9	241	7	US-11-096-568A-9945
21	215	5.9	245	7	US-11-096-568A-9944
22	215	5.9	280	7	US-11-096-568A-9943
23	215	5.9	2556	7	US-11-050-346-67
24	210	5.8	1719	7	US-11-234-786-378
25	209.5	5.8	656	7	US-11-234-786-379

26	209.5	5.8	671	7	US-11-234-786-380
27	208.5	5.8	657	7	US-11-072-512-2529
28	208.5	5.8	835	7	US-11-186-283-2
29	207	5.7	779	7	US-11-096-568A-1544
30	206.5	5.7	380	7	US-11-096-568A-3088
31	206.5	5.7	835	7	US-11-096-568A-3091
32	206.5	5.7	2471	7	US-11-186-283-8
33	205	5.6	329	7	US-11-050-346-68
34	202	5.6	382	7	US-11-234-786-376
35	201	5.6	384	7	US-11-096-568A-32354
36	201	5.6	384	7	US-11-096-568A-32353
37	197	5.4	292	7	US-11-234-786-532
38	196.5	5.4	596	7	US-11-072-512-2675
39	194	5.4	1554	7	US-11-186-284-93
40	190.5	5.3	456	7	US-11-096-568A-16313
41	190.5	5.3	461	7	US-11-096-568A-16312
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44	185.5	5.1	448	7	US-11-096-568A-11367
45	180	5.0	504	7	US-11-096-568A-10314

#### ALIGNMENTS

#### RESULT 1

US-10-055-877-139

; Sequence 139, Application US/10055877

; Publication No. US20050288241A1

; GENERAL INFORMATION:

; APPLICANT: DeCristofaro, Marc

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Miller, Charles

; APPLICANT: Tchernev, Velizar

; APPLICANT: Zhong, Mei

; APPLICANT: Anderson, David

; APPLICANT: Ballinger, Robert

; APPLICANT: Gerlach, Valerie

; APPLICANT: Spytek, Kimberly

; APPLICANT: Ratelli, Luca

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Guo, Xiaojia

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Andrew, David

; APPLICANT: Mezes, Peter

; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine

; APPLICANT: Eisen, Andrew

; APPLICANT: Wolenc, Adam

; APPLICANT: Baumgartner, Jason

; APPLICANT: Shimkets, Richard

; APPLICANT: Gusev, Vladimir

; APPLICANT: Vernet, Corine

; APPLICANT: Taupier Jr., Raymond

; APPLICANT: Pena, Carol

; APPLICANT: Shenoy, Suresh

; APPLICANT: Li, Li

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

; FILE REFERENCE: 21402-251

; CURRENT APPLICATION NUMBER: US/10/055,877

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/262,892

; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/263,598

; PRIOR FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 60/263,799

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/264,117

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/264,139

; PRIOR FILING DATE: 2001-01-25



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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-877-139

Query Match      8.6%; Score 310; DB 6; Length 1159;
Best Local Similarity 27.8%; Pred. No. 1.1e-19;
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

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DB 349 HVRVAKLLLD--RNADANARALNGFTPLHIAKKNRLKVVELLRL---HGASIS---A 398
QY 148 ENEEGCTPLHLACRKGDELVELVOYCHTQMDVTDYKGETVPHYAVQGDNSQVQLLGR 207
DB 399 TTESGUTPLHVAAFMGCMIVIVLQH--DASPDVPTVGETPLHLAARANQTDIIRILLR 457
QY 208 NAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCN-----247
DB 458 NG-AQVDARAREQQTPLHIASRLGNVDIVMLLQHGQVDATTKDMMYTAHLHIAKEGQDE 516
QY 248 ---IMPNG-----YPIHSAMKFSQKCAEMISMDSQIHSKDPHYGASPLHW 293
DB 517 VAAVLIENTGAALDAATKKGFTPLHLTAKYGHKIVQAQLLQKEADV--DAQGKNGVTPHLV 574
QY 294 A---KNAEWARMLLKGCNNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHG 350
DB 575 ACHYNNQVALLLEKGAHPATKNGHTPLHIAARKNQMDIATTLLEYGALANAEKAG 634
QY 351 NTPHLAMSKDNVEMIKALIVFGAEVDTNDFTGFTTFLASK 392
DB 635 FTPLHLSQEGHAEINLLIEHKAAVNHPAKNGLTPLHLCAQ 676

RESULT 2
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match      8.2%; Score 296; DB 6; Length 4384;
Best Local Similarity 29.2%; Pred. No. 1.7e-17;

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Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

QY 124 HLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDELVELVOYCHTQMDVTD 183
DB 511 HISARLGKADIVQQLLOQASPNAAATTSYTPHLHSAREGHEDVAAFLDHH--GASUSITT 569
QY 184 YKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCN 243
DB 570 KKGFTPLHVAAYKGLKLEAVANLLQKS--ASPDAAAGSKSLTPLHVAAHYDNQKVALLLDQ 628
QY 244 ARCNTMGPNY-PIHSAMKFSQKCAEMII--SMSSQIHSKDPHYGASPLHWAK---NA 297
DB 629 ASPHAAAKNGYTPHLHIAKKNQMDIATTLLEYGADANAV---TROGSIASVHLAAQEGHV 684
QY 298 ENARMLLKGCNNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLA 357
DB 685 DNVSILLGRNANVNLSKSGLTPLHLAQEDRVNVAEVLVNOGHVDAQTCKGYTTLHVG 744
QY 358 MSKDNVEMIKALIVFGAEVDTNDFTGFTTFLASKIG 394.
DB 745 CHYGNIKIVNFWLQHSKAVNAKTKNGYTPHLHQAQOG 781

RESULT 3
US-10-055-877-140
; Sequence 140, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 35.6667 Seconds  
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Title: US-10-612-668-21  
Perfect score: 3620  
Sequence: 1 MQFFGLVNTFSGVTNLFNSN.....GAKELGKVVDCCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3620	100.0	687	2	US-09-927-180-21
4	3606.5	99.6	688	1	US-08-555-568B-23
5	3606.5	99.6	688	2	US-09-519-223-23
6	3606.5	99.6	688	2	US-09-927-180-23
7	3566.5	98.5	819	2	US-09-949-016-10948
8	3302.5	91.2	752	1	US-08-281-193-2
9	3302.5	91.2	752	1	US-08-422-106-2
10	3302.5	91.2	752	1	US-08-735-716-2
11	3302.5	91.2	752	1	US-08-555-568B-2
12	3302.5	91.2	752	2	US-09-519-223-2
13	3302.5	91.2	752	2	US-09-927-180-2
14	3302.5	91.2	752	4	PCT-US95-08069-2
15	2084	57.6	394	1	US-08-555-568B-17
16	2084	57.6	394	2	US-09-519-223-17
17	2084	57.6	394	2	US-09-927-180-17
18	1531	42.3	292	1	US-08-555-568B-19
19	1531	42.3	292	2	US-09-519-223-19
20	1531	42.3	292	2	US-09-927-180-19
21	1163.5	32.1	896	2	US-09-270-767-46130
22	902.5	24.9	545	2	US-09-270-767-61684
23	371	10.2	143	2	US-09-270-767-33298
24	338	9.3	843	1	US-09-172-977-3
25	338	9.3	843	2	US-09-404-108-3
26	332	9.2	1839	1	US-09-172-977-4
27	332	9.2	1839	2	US-09-404-108-4

28	332	9.2	2753	2	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	2	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	2	US-09-538-092-1246	Sequence 1246, Ap
31	305.5	8.4	1745	1	US-09-031-485-33	Sequence 33, Appl
32	305.5	8.4	1745	1	US-08-847-429A-33	Sequence 33, Appl
33	305.5	8.4	1745	2	US-09-065-474-33	Sequence 33, Appl
34	305.5	8.4	1745	2	US-09-557-034-33	Sequence 33, Appl
35	302	8.3	786	2	US-09-509-802-2	Sequence 2, Appl
36	302	8.3	787	2	US-09-188-930-334	Sequence 334, App
37	302	8.3	787	2	US-09-312-283C-334	Sequence 334, App
38	300.5	8.3	1724	2	US-09-964-899-43	Sequence 43, Appl
39	296	8.2	1088	2	US-09-082-059-2	Sequence 2, Appli
40	296	8.2	3913	2	US-09-949-016-10933	Sequence 10933, A
41	296	8.2	4377	2	US-09-949-016-6978	Sequence 6978, Ap
42	294	8.1	1719	2	US-09-949-016-6966	Sequence 6966, Ap
43	294	8.1	1856	2	US-09-949-016-6964	Sequence 6964, Ap
44	294	8.1	1880	2	US-09-949-016-5876	Sequence 5876, Ap
45	294	8.1	1881	2	US-09-949-016-6965	Sequence 6965, Ap

ALIGNMENTS

RESULT 1  
US-08-555-568B-21  
; Sequence 21, Application US/085555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-21

Query Match	100.0%;	Score 3620;	DB 1;	Length 687;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 687;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MQFFGLVNTSGVTNLFNSNPRVKVAVADYTS	SDRVREGQLILFQNTPNRTWDCVLV	60
QY	61	NPRNSQSGRFLFOLEADALVNFHQYSSQLLPFY	ESSPQVLHTEVQLHLDLRNHPWS	120
Db	61	NPRNSQSGRFLFOLEADALVNFHQYSSQLLPFY	ESSPQVLHTEVQLHLDLRNHPWS	120

121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
181 VTDYKGETVHYAVOGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
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361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGKQLDLMHISRARKPAFIIIGSMRDEKR 420  
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421 THDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHKSMA 480  
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481 YMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGHTKMTDVRKPKVMTGTILSDROPAPAE 540  
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541 LHLFRNYDAPETVREPRFNQVNLPPAOPSDOLVWRAARSSGAAPTYFRPNRGRFDGGL 600  
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661 ELAKTVFGAKELGKMVVDCTDPDGRP 687  
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## RESULT 2

US-09-519-223-21  
; Sequence 21, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO. 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-519-223-21

Query Match 100.0%; Score 3620; DB 2; Length 687;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADTSSDRVREGQLILFQNTPRNTWDCVLV 60  
QY 61 NPNRSQSGFRLQFLEADALVNFHQYSSQLLPFYESSPQVLHTEVLQHLTLIRNHPSW 120  
DB 61 NPNRSQSGFRLQFLEADALVNFHQYSSQLLPFYESSPQVLHTEVLQHLTLIRNHPSW 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
QY 181 VTDYKGETVHYAVOGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVHYAVOGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCNIMPGNYPYIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
DB 241 LCNARCNIMPGNYPYIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGKQLDLMHISRARKPAFIIIGSMRDEKR 420  
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGKQLDLMHISRARKPAFIIIGSMRDEKR 420  
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DB 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGHTKMTDVRKPKVMTGTILSDROPAPAE 540  
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DB 541 LHLFRNYDAPETVREPRFNQVNLPPAOPSDOLVWRAARSSGAAPTYFRPNRGRFDGGL 600  
QY 601 LANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNPW 660  
DB 601 LANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNPW 660  
QY 661 ELAKTVFGAKELGKMVVDCTDPDGRP 687  
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## RESULT 3

US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 120.175 Seconds  
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2392.073 Million cell updates/sec

Title: US-10-612-668-23  
Perfect score: 3625  
Sequence: 1 MQFFGLVNTFSGVTNLFNSN.....GAKELGRMVVDCCTDPDRP 688

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	3315	91.4	752	5	US-10-612-668-2
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13	651	18.0	1071	4	US-10-369-493-6865
14	627	17.3	1023	4	US-10-369-493-6689
15	627	17.3	1023	4	US-10-369-493-6690
16	326	9.0	468	4	US-10-369-493-4998
17	324	8.9	1330	4	US-10-108-260A-3237
18	319.5	8.8	1549	6	US-11-097-143-1776
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22	301.5	8.3	786	4	US-10-299-327-2
23	301.5	8.3	786	4	US-10-128-174-13
24	301.5	8.3	786	4	US-10-128-174-31
25	301.5	8.3	786	4	US-10-128-174-32
26	301.5	8.3	786	4	US-10-128-174-33
27	301.5	8.3	787	3	US-09-866-050A-334

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29	301.5	8.3	1724	5	US-10-975-523-43	Sequence 43, Appl
30	301	8.3	347	4	US-10-128-174-30	Sequence 30, Appl
31	296	8.2	1094	5	US-10-479-764-22	Sequence 22, Appl
32	296	8.2	1097	5	US-10-450-763-52300	Sequence 52300, A
33	296	8.2	3913	4	US-10-334-143-45	Sequence 45, Appl
34	296	8.2	4274	5	US-10-450-763-31331	Sequence 31331, A
35	296	8.2	4377	5	US-10-756-149-4917	Sequence 4917, Ap
36	296	8.2	4386	5	US-10-450-763-37734	Sequence 37734, A
37	296	8.2	4397	5	US-10-450-763-52303	Sequence 52303, A
38	293.5	8.1	1762	4	US-10-205-194-117	Sequence 117, App
39	286.5	7.9	720	4	US-10-433-794-20	Sequence 20, Appl
40	286.5	7.9	765	4	US-10-128-174-3	Sequence 3, Appli
41	286.5	7.9	765	4	US-10-128-174-34	Sequence 34, Appl
42	286.5	7.9	765	4	US-10-128-174-35	Sequence 35, Appl
43	286.5	7.9	765	4	US-10-128-174-36	Sequence 36, Appl
44	286.5	7.9	765	4	US-10-128-174-37	Sequence 37, Appl
45	286.5	7.9	765	4	US-10-128-174-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-927-180-23  
; Sequence 23, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 688 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-927-180-23

Query Match 100.0%; Score 3625; DB 3; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTPNRTDCVLV 60  
DB 1 MQFFGLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREGQLILFQNTPNRTDCVLV 60

QY 61 NPNSSQSGFRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
DB 61 NPNSSQSGFRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
QY 181 VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLODLMHISRAKPAFILGSMRDEK 420  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLODLMHISRAKPAFILGSMRDEK 420  
QY 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
DB 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
QY 481 AYMRGMYFRMKDEVRFGSRPYESGLEEFKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540  
DB 481 AYMRGMYFRMKDEVRFGSRPYESGLEEFKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540  
QY 541 ELHLFRNYDAPETVREPRNQVNLPPAOPSQDLVWRAARSSGAAPTFRNGRFLDGG 600  
DB 541 ELHLFRNYDAPETVREPRNQVNLPPAOPSQDLVWRAARSSGAAPTFRNGRFLDGG 600  
QY 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
DB 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
QY 661 WELAKTVFGAKELGKMVDCCTDPDGRP 688  
DB 661 WELAKTVFGAKELGKMVDCCTDPDGRP 688

## RESULT 2

US-10-612-668-23

Sequence 23, Application US/10612668

Publication No. US20050196852A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridge Park Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/612,668

FILING DATE: 01-Jul-2003

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

## RESULT 3

US-09-927-180-21

FILING DATE: 09-Aug-2001  
APPLICATION NUMBER: 09/519,223  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 688 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-612-668-23

Query Match 100.0%; Score 3625; DB 5; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREGQLILFQNTPTNRTWDCVLV 60  
QY 61 NPNSSQSGFRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
DB 61 NPNSSQSGFRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRCFHHSRIISCANCAENEBEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
QY 181 VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLODLMHISRAKPAFILGSMRDEK 420  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLODLMHISRAKPAFILGSMRDEK 420  
QY 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
DB 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
QY 481 AYMRGMYFRMKDEVRFGSRPYESGLEEFKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540  
DB 481 AYMRGMYFRMKDEVRFGSRPYESGLEEFKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540  
QY 541 ELHLFRNYDAPETVREPRNQVNLPPAOPSQDLVWRAARSSGAAPTFRNGRFLDGG 600  
DB 541 ELHLFRNYDAPETVREPRNQVNLPPAOPSQDLVWRAARSSGAAPTFRNGRFLDGG 600  
QY 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
DB 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
QY 661 WELAKTVFGAKELGKMVDCCTDPDGRP 688  
DB 661 WELAKTVFGAKELGKMVDCCTDPDGRP 688

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 15.0218 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622899 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	8.6	1159	6	US-10-055-877-139
2	296	8.2	1765	6	US-10-055-877-140
3	296	8.2	1940	6	US-10-055-877-141
4	296	8.2	4384	6	US-10-821-234-1120
5	281	7.8	784	7	US-11-072-175-153
6	271.5	7.5	1059	6	US-10-055-877-138
7	263.5	7.3	1431	6	US-10-501-035-220
8	252	7.0	795	7	US-11-072-512-2378
9	249	6.9	737	6	US-10-055-877-137
10	244	6.7	237	7	US-11-096-568A-28113
11	244	6.7	247	7	US-11-096-568A-28112
12	238	6.6	831	7	US-11-096-568A-1542
13	236	6.5	993	6	US-10-055-877-6
14	233	6.4	784	7	US-11-096-568A-22417
15	229.5	6.3	240	7	US-11-096-568A-22416
16	229.5	6.3	244	7	US-11-096-568A-22416
17	229.5	6.3	645	7	US-11-072-512-2588
18	227	6.3	505	7	US-11-072-512-2553
19	223	6.2	219	7	US-11-096-568A-28114
20	214.5	5.9	241	7	US-11-096-568A-9945
21	214.5	5.9	245	7	US-11-096-568A-9944
22	214.5	5.9	280	7	US-11-096-568A-9943
23	211.5	5.8	657	7	US-11-072-512-2529
24	209.5	5.8	1719	7	US-11-234-786-378
25	209.5	5.8	2471	7	US-11-050-346-68

Sequence 379, App  
Sequence 380, App  
Sequence 67, Appl  
Sequence 1544, Ap  
Sequence 8, Appl  
Sequence 3088, Ap  
Sequence 3091, Ap  
Sequence 2, Appl  
Sequence 376, App  
Sequence 32354, A  
Sequence 32353, A  
Sequence 2675, Ap  
Sequence 532, App  
Sequence 16313, A  
Sequence 16312, A  
Sequence 11369, A  
Sequence 11368, A  
Sequence 11367, A  
Sequence 93, Appl  
Sequence 975, App

#### ALIGNMENTS

RESULT 1  
US-10-055-877-139  
; Sequence 139, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:

; APPLICANT: DeCristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512.
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 139
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-877-139

Query Match      8.6%; Score 310; DB 6; Length 1159;
Best Local Similarity 27.8%; Pred. No. 1.6e-19;
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

QY 103 HTEVLOHLTDLRNHP-----WSVAHLA-----VELGIRECFHHSRIISCANCA 147
DB 349 HVRVAKLLD--RNADANARALNGFTPLHACKNRLKVVELLR-----HGASIS---A 398

QY 148 ENEEGCTPLHLACKRGDGEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLLGLR 207
DB 399 TTESGLTPLHVAFAFMCMNIVLYLQH--DASPDPVTVRGETPLHLAARANQTDIIRLLR 457

QY 208 NAVAGLNQVNNQGLTPLHLACOLGKQEMVRVILLNCARN-----247
DB 458 NG-AQVDARAREQOTPLHTASRLGNVDIVMLLQHGQAVDATTKDMYTALHTAAKEGQDE 516

QY 248 ----IMGPNG-----YPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHW 293
DB 517 VAAVLIENTGAALDAATKKGFTPLHLTAKYGHKVAQLLQKEADV--DAQGKNGVTPLHV 574

QY 294 A----KNAEMARMLLKGCNVNSTSSAGNTALHVGVMNRPDCAIVLLTHGANADARGEHG 350
DB 575 ACHYNNQVALLLEKGSAPHATAKNGHTPLHTAARKNQMDIATTLLEYGALANAESKAG 634

QY 351 NTPHLAMSKDNVEMIKALIVFGAEYDTPNDFGETPTFLASK 392
DB 635 FTPLHLSQSGRAEISNLLIEHKAAVNHFAKNGLTTPMHLCAQ 676

RESULT 2
US-10-055-877-140
; Sequence 140, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Fatturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
```

```
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 140
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-140

Query Match      8.2%; Score 296; DB 6; Length 1765;
Best Local Similarity 24.7%; Pred. No. 5.8e-18;
Matches 112; Conservative 82; Mismatches 191; Indels 68; Gaps 18;

QY 124 HLAVELG----IRECFHHSRIISCANCAENEGCTPLHLACKRGDGEILVELVQYCHTQM 179
DB 421 HVAAFMGHVNTVSQMLMH---GASPNTTNRGETPLHMAARSGQAEVVRYLVQ--DGAQV 475

QY 180 DVTDYKGETVFHYAVQGDNSQVLOLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVL 239
DB 476 EAKAKDDQTPHISARLGKADIVQQLQOG--ASPNAATTSYGTPLHLAAREGHEDVAAPFL 534

QY 240 LLCNARNIMGPNGY-PIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWA---K 295
DB 535 LDHGASLSITTKKGFTPLHVAAYKGLVVASLLOKSASP--DAAGKSGLTPLHVAAYHD 592

QY 296 NAEMARMLLKGCNVNSTSSAGNTALHVGVMNRPDCAIVLLTHGANADARGEHNTPLH 355
DB 593 NQVALLLLDQGSAPHAANKNGYTPHLTAARKNQMDIATSLLEYGADANAVTROGIASVH 652

QY 356 LAMSKDNVEMIKALIVFGAEYDTPNDFGETPTFLASKIGR-OLQDLM-----HISRARKP 409
DB 653 LAAQEGHVDVMSLLSRNANVLSNKSGLTPLHLAAQEDRVNVAEVLVNOGHAVDAQTGM 712

QY 410 AFILGSMRDEKRTDHLCLDGGGVKGLIIIIQLLIAIKASGVATKDLFDWVAGTSTGCI 469
DB 713 GV-----TPLHVGCHYGNIK---IVNFLQHSKAKVNAKTKN-----GY 747

QY 470 LALAILHKSMAVMYRMGMFRMKDEVFRGSRPYE---SGPLEEFLKREGEHTKMTDVRK- 525
DB 748 TAL-----HQAQQGHTHIIINVLLQNNASPNELTVNGNTALAIARLLG-YISVVDTLKV 800
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

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1592.473 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

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Scoring table: BLOSUM62

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3625	100.0	688	1 US-08-555-568B-23	Sequence 23, Appl
2	3625	100.0	688	2 US-09-519-223-23	Sequence 23, Appl
3	3625	100.0	688	2 US-09-927-180-23	Sequence 23, Appl
4	3606.5	99.5	687	1 US-08-555-568B-21	Sequence 21, Appl
5	3606.5	99.5	687	2 US-09-519-223-21	Sequence 21, Appl
6	3606.5	99.5	687	2 US-09-927-180-21	Sequence 21, Appl
7	3572	98.5	819	2 US-09-949-016-10948	Sequence 10948, A
8	3315	91.4	752	1 US-08-281-193-2	Sequence 2, Appl
9	3315	91.4	752	1 US-08-422-106-2	Sequence 2, Appl
10	3315	91.4	752	1 US-08-735-716-2	Sequence 2, Appl
11	3315	91.4	752	1 US-08-555-568B-2	Sequence 2, Appl
12	3315	91.4	752	2 US-09-519-223-2	Sequence 2, Appl
13	3315	91.4	752	2 US-09-927-180-2	Sequence 2, Appl
14	3315	91.4	752	4 PCT-US95-08069-2	Sequence 2, Appl
15	2084	57.5	394	1 US-08-555-568B-17	Sequence 17, Appl
16	2084	57.5	394	2 US-09-519-223-17	Sequence 17, Appl
17	2084	57.5	394	2 US-09-927-180-17	Sequence 17, Appl
18	1531	42.2	292	1 US-08-555-568B-19	Sequence 19, Appl
19	1531	42.2	292	2 US-09-519-223-19	Sequence 19, Appl
20	1531	42.2	292	2 US-09-927-180-19	Sequence 19, Appl
21	1165	32.1	896	2 US-08-270-767-46130	Sequence 46130, A
22	904	24.9	545	2 US-09-270-767-61684	Sequence 61684, A
23	371	10.2	143	2 US-09-270-767-33298	Sequence 33298, A
24	338	9.3	843	1 US-09-172-977-3	Sequence 3, Appl
25	338	9.3	843	2 US-09-404-108-3	Sequence 3, Appl
26	332	9.2	1839	1 US-09-172-977-4	Sequence 4, Appl
27	332	9.2	1839	2 US-09-404-108-4	Sequence 4, Appl

28 332 9.2 2753 2 US-09-949-016-7659 Sequence 7659, Ap  
29 332 9.2 2753 2 US-09-949-016-7660 Sequence 7660, Ap  
30 332 9.2 3924 2 US-09-538-092-1246 Sequence 1246, Ap  
31 308.5 8.5 1745 1 US-08-031-485-33 Sequence 33, Appl  
32 308.5 8.5 1745 1 US-08-847-429A-33 Sequence 33, Appl  
33 308.5 8.5 1745 2 US-08-065-474-33 Sequence 33, Appl  
34 308.5 8.5 1745 2 US-09-557-034-33 Sequence 33, Appl  
35 301.5 8.3 786 2 US-09-509-802-2 Sequence 2, Appl  
36 301.5 8.3 787 2 US-09-188-930-334 Sequence 334, App  
37 301.5 8.3 787 2 US-09-312-283C-334 Sequence 334, App  
38 301.5 8.3 1724 2 US-09-964-899-43 Sequence 43, Appl  
39 296 8.2 1088 2 US-09-082-059-2 Sequence 2, Appl  
40 296 8.2 3913 2 US-09-949-016-10933 Sequence 10933, A  
41 296 8.2 4377 2 US-09-949-016-6978 Sequence 6978, Ap  
42 294 8.1 1719 2 US-09-949-016-6966 Sequence 6966, Ap  
43 294 8.1 1856 2 US-09-949-016-6964 Sequence 6964, Ap  
44 294 8.1 1880 2 US-09-949-016-5876 Sequence 5876, Ap  
45 294 8.1 1881 2 US-09-949-016-6965 Sequence 6965, Ap

#### ALIGNMENTS

RESULT 1  
US-08-555-568B-23  
; Sequence 23, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 688 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-555-568B-23

Query Match 100.0%; Score 3625; DB 1; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQFFGLVNTFSGVTNLFNSPFVKEVAVADYSSDRVREEGQLILFQNTFNRTRDCLV 60  
DB 1 MQFFGLVNTFSGVTNLFNSPFVKEVAVADYSSDRVREEGQLILFQNTFNRTRDCLV 60  
QY 61 NPNRNSGGFRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLOHLDLIRNPSW 120  
DB 61 NPNRNSGGFRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLOHLDLIRNPSW 120



121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVOYCHTOMD 180  
121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVOYCHTOMD 180  
181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240  
181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240  
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241 LCNARCNIMGPNVGYPHSAKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMA 300  
301 RMLLKRCNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGTPLHLAMSK 360  
301 RMLLKRCNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGTPLHLAMSK 360  
361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQQLDMHISRARKPAFILGSRDEK 420  
361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQQLDMHISRARKPAFILGSRDEK 420  
421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480  
421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480  
481 AYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 540  
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541 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSQDLVWRAARSSGAAPTFRPNRFLDGG 600  
601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688  
661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

## RESULT 2

US-09-519-223-23  
; Sequence 23, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 688 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-519-223-23

Query Match 100.0%; Score 3625; DB 2; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADTSSDRVREEGQLILFQNTPNRTWCVLV 60  
DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADTSSDRVREEGQLILFQNTPNRTWCVLV 60  
QY 61 NPNRSQSGFRLFQLEADALVNFHYSSQLLPFYESSQVLTHTVLOHLDLIRNHPWS 120  
DB 61 NPNRSQSGFRLFQLEADALVNFHYSSQLLPFYESSQVLTHTVLOHLDLIRNHPWS 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVOYCHTOMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVOYCHTOMD 180  
QY 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240  
DB 181 VTDYKGETVPHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240  
QY 241 LCNARCNIMGPNVGYPHSAKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIMGPNVGYPHSAKFSQKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRCNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGTPLHLAMSK 360  
DB 301 RMLLKRCNVTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGTPLHLAMSK 360  
QY 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQQLDMHISRARKPAFILGSRDEK 420  
DB 361 DNVEIMKALIVFGAEVDTNDPGETPTFLASKIGRQQLDMHISRARKPAFILGSRDEK 420  
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480  
DB 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480  
QY 481 AYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 540  
DB 481 AYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 540  
QY 541 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSQDLVWRAARSSGAAPTFRPNRFLDGG 600  
DB 541 ELHLFRNYDAPETVREPRFNQVNLPRPAQPSQDLVWRAARSSGAAPTFRPNRFLDGG 600  
QY 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
DB 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688  
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

## RESULT 3

US-09-927-180-23  
; Sequence 23, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25